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Sequence Listing was accepted with existing errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Wed Jun 06 20:00:09 EDT 2007

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Application No: 10808538 Version No: 2.1

Input Set:

Output Set:

Started: 2007-06-06 20:00:01.170
Finished: 2007-06-06 20:00:02.426
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 256 ms
Total Warnings: 33
Total Errors: 0
No. of SeqIDs Defined: 45
Actual SeqID Count: 45

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W 213	Artificial or Unknown found in <213> in SEQ ID (31)

Input Set:

Output Set:

Started: 2007-06-06 20:00:01.170
Finished: 2007-06-06 20:00:02.426
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 256 ms
Total Warnings: 33
Total Errors: 0
No. of SeqIDs Defined: 45
Actual SeqID Count: 45

Error code	Error Description
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SEQUENCE LISTING

<110> Immunomedics, Inc.

Leung, Shui-on

Losman, Michele J.

Hansen, Hans

<120> HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC ANTIGEN ANTI-IDIOTYPE
ANTIBODY AS A TUMOR VACCINE AND FOR TARGETING APPLICATIONS

<130> 329329

<140> 10/808,538

<141> 2004-03-25

<150> US 09/155,106

<151> 1998-11-17

<150> PCT/US97/04696

<151> 1997-03-19

<150> US 60/013,708

<151> 1996-03-20

<160> 45

<170> PatentIn version 3.4

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<400> 1

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<210> 2

<211> 17

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35 40 45

Ala Xaa
50 55 60

Xaa Xaa Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
65 70 75 80

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Ala Arg Xaa Trp
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20

25

30

Trp Met Thr Trp Ile Arg Gln Ala Pro Gly Glu Gly Leu Glu Trp Val
35 40 45

Ala Ser Ile Thr Ser Thr Gly Gly Thr Tyr His Ala Glu Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Ser Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Thr Tyr Tyr Cys
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35 40 45

Ala Ser Ile Thr Ser Thr Gly Gly Thr Tyr His Ala Glu Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
65 70 75 80

Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Tyr Cys
85 90 95

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Gly Gln Gly Thr Pro Val Thr Val Ser Ser
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20 25 30

Trp Met Thr Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Ser Ile Thr Ser Thr Gly Gly Thr Tyr His Ala Glu Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
65 70 75 80

Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Tyr Cys
85 90 95

Ser Arg Asp Asp Tyr Gly Gly Gln Ser Thr Tyr Val Met Asp Ala Trp
100 105 110

Gly Gln Gly Thr Pro Val Thr Val Ser Ser
115 120

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Asp Arg Val Thr Ile Thr Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Trp Tyr Gln Gln Thr Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Xaa Xaa Xaa Xaa Xaa Xaa Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95

Xaa Phe Gly Gln Gly Thr Lys Leu Gln Ile Thr Arg Thr
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<210> 22
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<400> 22

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Leu Arg Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Thr Asn Leu Ala Ala Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Arg Ser Gly Ser Asp Phe Ser Leu Thr Ile Asn Ser Leu Glu Ser
65 70 75 80

Glu Asp Met Ala Ile Tyr Tyr Cys Leu His His Ser Glu Tyr Pro Tyr
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Thr Phe Gly Ile Gly Thr Lys Leu Glu Arg Lys Arg
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20 25 30

Leu Arg Trp Phe Gln Gln Thr Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Gly Ala Thr Asn Leu Ala Ala Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Arg Ser Gly Ser Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
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Glu Asp Ile Ala Thr Tyr Tyr Cys Leu His His Ser Glu Tyr Pro Tyr

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90

95

Thr Phe Gly Ile Gly Thr Lys Leu Gln Ile Lys Arg
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20 25 30

Leu Arg Trp Phe Gln Gln Thr Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Gly Ala Thr Asn Leu Ala Ala Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Leu His His Ser Glu Tyr Pro Tyr
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Thr Phe Gly Ile Gly Thr Lys Leu Gln Ile Lys Arg
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ccagggaaagg gtcttgaatg ggttgcgtcc attactagta ctggtggtgg tacctaccat 180
gcagagtctg tgaaggggccg attcactatc tccagagata attcaaaaaa caccctgttc 240
ctgcaaatgg acagtctgag gcctgaggac acgggcgtt attactgttc aagagatgac 300
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20 25 30

Trp Met Thr Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Ser Ile Thr Ser Thr Gly Gly Thr Tyr His Ala Glu Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
65 70 75 80

Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Tyr Cys
85 90 95

Ser Arg Asp Asp Tyr Gly Gly Gln Ser Thr Tyr Val Met Asp Ala Trp
100 105 110

Gly Gln Gly Thr Pro Val Thr Val Ser Ser
115 120

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gggaaagctc cgaaactttt gatttatggt gcaaccaact tggctgcagg ggtcccatca	180
cggttcagtg gcagtggtc tgggacagat tttactttta ccatctcaag ctttcagcct	240
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gggaccaagt tgcagatcaa acgtg	325

<210> 28

<211> 108

<212> PRT

<213> Artificial

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<223> REIWI2VK Sequence

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Gly Asn Tyr		
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Leu Arg Trp Phe Gln Gln Thr Pro Gly Lys Ala Pro Lys Leu Leu Ile		
35	40	45

Tyr Gly Ala Thr Asn Leu Ala Ala Gly Val Pro Ser Arg Phe Ser Gly		
50	55	60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro			
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cgttcaagtc gcagtaggtc tgggtcagat ttttctctga ccatcaacag cctggagtct 240

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<210> 30

<211> 108

<212> PRT

<213> Rat

<400> 30

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Gly Asn Tyr
20 25 30

Leu Arg Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Thr Asn Leu Ala Ala Gly Val Pro Ser Arg Phe Ser Arg
50 55 60

Ser Arg Ser Gly Ser Asp Phe Ser Leu Thr Ile Asn Ser Leu Glu Ser
65 70 75 80

Glu Asp Met Ala Ile Tyr Tyr Cys Leu His His Ser Glu Tyr Pro Tyr
85 90 95

Thr Phe Gly Ile Gly Thr Lys Leu Glu Arg Lys Arg
100 105

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